

**AMENDMENTS TO THE CLAIMS:**

Claims 29-43 are canceled without prejudice or disclaimer. Claims 44-75 are added. The following is the status of the claims of the above-captioned application, as amended.

Claims 1-43 (Canceled).

Claim 44 (New). A variant of a parent Glycoside Hydrolase Family 53 galactanase, comprising an alteration in at least one of the following positions:

90, 91, 181, 303, 305, and 313,

wherein

(a) the parent Glycoside Hydrolase Family 53 galactanase comprises an amino acid sequence which is at least 80% identical to SEQ ID NO: 1;

(b) the variant comprises an amino acid sequence which is at least 80% identical to SEQ ID NO: 1;

(c) each position is the number of the corresponding amino acid residue in SEQ ID NO: 1;

(d) the alteration(s) are independently

(i) an insertion of an amino acid immediately downstream of the position,

(ii) a deletion of the amino acid which occupies the position, and/or

(iii) a substitution of the amino acid which occupies the position; and

(e) the variant has galactanase activity.

Claim 45 (New). The variant of claim 44, wherein the alteration(s) are substitutions.

Claim 46 (New). The variant of claim 44, wherein the parent Glycoside Hydrolase Family 53 galactanase comprises an amino acid sequence which is at least 85% identical to SEQ ID NO: 1.

Claim 47 (New). The variant of claim 44, wherein the parent Glycoside Hydrolase Family 53 galactanase comprises an amino acid sequence which is at least 90% identical to SEQ ID NO: 1.

Claim 48 (New). The variant of claim 44, wherein the parent Glycoside Hydrolase Family 53 galactanase comprises an amino acid sequence which is at least 95% identical to SEQ ID NO: 1.

Claim 49 (New). The variant of claim 44, wherein the variant comprises an amino acid sequence which is at least 85% identical to SEQ ID NO: 1.

Claim 50 (New). The variant of claim 44, wherein the variant comprises an amino acid sequence which is at least 90% identical to SEQ ID NO: 1.

Claim 51 (New). The variant of claim 44, wherein the variant comprises an amino acid sequence which is at least 95% identical to SEQ ID NO: 1.

Claim 52 (New). The variant of claim 44, which comprises an alteration at position 90.

Claim 53 (New). The variant of claim 52, wherein the variant comprises:  
90A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y.

Claim 54 (New). The variant of claim 53, wherein the variant comprises:  
90A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,T,V,W,Y.

Claim 55 (New). The variant of claim 44, which comprises an alteration at position 91.

Claim 56 (New). The variant of claim 55, wherein the variant comprises:  
91A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y.

Claim 57 (New). The variant of claim 44, which comprises an alteration at position 181.

Claim 58 (New). The variant of claim 57, wherein the variant comprises:  
181A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y.

Claim 59 (New). The variant of claim 44, which comprises an alteration at position 303.

Claim 60 (New). The variant of claim 59, wherein the variant comprises:

303A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y.

Claim 61 (New). The variant of claim 44, which comprises an alteration at position 305.

Claim 62 (New). The variant of claim 61, wherein the variant comprises:

305A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y.

Claim 63 (New). The variant of claim 44, which comprises an alteration at position 313.

Claim 64 (New). The variant of claim 63, wherein the variant comprises:

313A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y.

Claim 65 (New). The variant of claim 44, wherein the variant comprises at least one of the following substitutions:

(a) Y214N,S+N247Y+L306Q; Y214A; F216FVASTG; and/or P89W+W86N;

(b) A90S+H91D; H91N,L,D; N313D; N303D,H; and/or N305D,H;

(c) Y22P, N24P, T25P, A29P, A53P, N56P, T93P, D101P, W142P, T147P, Q198P, L203P, S204P, S219P, S258P, S288P, A304P, A311P, Q318P, A322P, S324P, S325P, and/or S327P;

(d) W107S,H;

(e) Q126E;

(f) N39C+L326C; V20C+G320C; Y110C+G163C; W150C+N194C; T274C+V328C;

and/or I301C+F316C; and/or

(g) A90C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;

H91A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;

N181A,C,D,E,F,G,H,I,K,L,M,P,Q,R,S,T,V,W,Y;

N303A,C,D,E,F,G,H,I,K,L,M,P,Q,R,S,T,V,W,Y;

N305A,C,D,E,F,G,H,I,K,L,M,P,Q,R,S,T,V,W,Y; and/or

N313A,C,D,E,F,G,H,I,K,L,M,P,Q,R,S,T,V,W,Y.

Claim 66 (New). The variant of claim 65, which is a variant of a *Myceliophthora thermophila* galactanase.

Claim 67 (New). The variant of claim 44, wherein the variant comprises at least one of the following substitutions:

(a) V20P, V25P, E29P, V41P, V50P, W53P, N56P, T94P, A96P, W142P, L169P, W185P, Q198P, M203P, A219P, A221P, T222P, Q258P, A261P, D262P, S288P, N305P, A311P, A322P, S324P, and/or S325P;

(b) T113C+G163C, W185C+S229C, S218C+A221C, R227C+V283C; and/or

(c) A90C,D,E,F,G,H,I,J,K,L,M,N,P,Q,R,S,T,V,W,Y;

H91A,C,D,E,F,G,H,I,J,K,L,M,N,P,Q,R,S,T,V,W,Y;

N181A,C,D,E,F,G,H,I,J,K,L,M,P,Q,R,S,T,V,W,Y;

N303A,C,D,E,F,G,H,I,J,K,L,M,P,Q,R,S,T,V,W,Y;

N305A,C,D,E,F,G,H,I,J,K,L,M,P,Q,R,S,T,V,W,Y; and/or

N313A,C,D,E,F,G,H,I,J,K,L,M,P,Q,R,S,T,V,W,Y.

Claim 68 (New). The variant of claim 67, which is a variant of a *Humicola insolens* galactanase.

Claim 69 (New). The variant of claim 44, wherein the variant comprises at least one of the following substitutions:

(a) D181N, D181N+S90A+D91H;

(b) T3P, Y20P, N24P, L25P, T29P, A31P, V50P, S53P, S56P, T93P, T94P, S96P, W142P, L144P, E146P, T147P, T172P, E200P, S203P, A219P, A256P, A258P, S261P, S264P, I266P, T288P, I301P, A304P, Y318P, and/or E324P;

(c) L13C+L65C, N24C+Q30C, S218C+A221C, A304C+Y318C; and/or

(d) S90A,C,D,E,F,G,H,I,K,L,M,N,P,Q,R,T,V,W,Y;

D91A,C,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;

D181A,C,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;

N303A,C,D,E,F,G,H,I,K,L,M,P,Q,R,S,T,V,W,Y;

G305A,C,D,E,F,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; and/or

N313A,C,D,E,F,G,H,I,K,L,M,P,Q,R,S,T,V,W,Y; and/or

(e) I9F,Y,W; L12V; L80F; L82Y; F191Y,W; Y213F; I9W+L12V; L82Y+L80F.

Claim 70 (New). The variant of claim 69, which is a variant of an *Aspergillus aculeatus* galactanase.

Claim 71 (New). The variant of claim 44, wherein the variant comprises at least one of the following substitutions:

(a) K-6P, S-4P, L-2P, K1P, V20P, S26P, K29P, D31P, A54aP, G54eP, N57P, K93P, A97P, N101P, S171P, S185P, T256P, N260P, N266P, D286P, E288aP, A289P, A302dP, S302yP, Y302zP, A302bbP, E302ccP, E302ggP, F305P, D311P, F318P;

(b) S18C+Y302qC, G40C+Q330C, V44C+A69C, I48C+A62C, N50C+D84C, G54gC+T302xC, N56C+G302rC, A62C+G146C, K106C+A159C, K114C+A163C, E183C+G221C, T227C+A283C, A234C+V241C, Y250C+Q273C, A302aaC+A302iiC; and/or

(c) A90C,D,E,F,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y;  
K91A,C,D,E,F,G,H,I,L,M,N,P,Q,R,S,T,V,W,Y;  
N181A,C,D,E,F,G,H,I,K,L,M,P,Q,R,S,T,V,W,Y;  
K303A,C,D,E,F,G,H,I,L,M,N,P,Q,R,S,T,V,W,Y;  
F305A,C,D,E,G,H,I,K,L,M,N,P,Q,R,S,T,V,W,Y; and/or  
Q313A,C,D,E,F,G,H,I,K,L,M,N,P,R,S,T,V,W,Y.

Claim 72 (New). The variant of claim 71, which is a variant of a *Bacillus licheniformis* galactanase.

Claim 73 (New). The variant of claim 44, wherein the parent galactanase is obtained from a strain of *Aspergillus*, *Bacillus*, *Bifidobacterium*, *Cellvibrio*, *Clostridium*, *Humicola*, *Meripilus*, *Myceliophthora*, *Pseudomonas*, *Thermomyces*, *Thermotoga*, *Xanthomonas*, or *Yersinia*.

Claim 74 (New). An animal feed composition, comprising a variant of claim 44.

Claim 75 (New). A method for hydrolyzing lactose, comprising treating the lactose with a galactanase variant of claim 44.